



## SEQUENCE LISTING

#5

<110> Millennium Pharmaceuticals, Inc.  
Glucksmann, Maria  
Tsai, Fong-Ying

<120> 27439, NOVEL HUMAN HYDROXYLASE AND USES  
THEREFOR

<130> 38155-20036.00

<140> US 09/945,301

<141> 2001-08-31

<150> US 60/229,301

<151> 2000-09-01

<160> 16

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1976

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1614)

<221> misc\_feature

<222> (1)...(1976)

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gag cgg ggt ggg ctc ctg ggc ggc ggg gcc ccg cgg cgg cct caa ccc 96  
Glu Arg Gly Gly Leu Leu Gly Gly Gly Ala Pro Arg Arg Pro Gln Pro  
20 25 30

gcg ggc gca cgg ctc ccg gcg ggg gcg cgg gcc gag gac aaa ggc gcc 144  
Ala Gly Ala Arg Leu Pro Ala Gly Ala Arg Ala Glu Asp Lys Gly Ala  
35 40 45

ggg cgg ccg ggg tcg ccg ccg gga ggg ggc cga gcc gag ggt ccc cgg 192  
Gly Arg Pro Gly Ser Pro Pro Gly Gly Gly Arg Ala Glu Gly Pro Arg  
50 55 60

agc ctc gcc gcc atg ccg ggg ccg agg acc ctc gcc aac ctg gcg gag 240  
Ser Leu Ala Ala Met Pro Gly Pro Arg Thr Leu Ala Asn Leu Ala Glu  
65 70 75 80

ttc ttc tgc agg gac ggc ttc agc cgc atc cac gag atc cag cag aag 288

Phe	Phe	Cys	Arg	Asp	Gly	Phe	Ser	Arg	Ile	His	Glu	Ile	Gln	Gln	Lys	
				85					90					95		
cac	aca	cgg	gaa	tat	gga	aaa	atc	ttc	aag	tct	cac	ttt	ggg	cct	cag	336
His	Thr	Arg	Glu	Tyr	Gly	Lys	Ile	Phe	Lys	Ser	His	Phe	Gly	Pro	Gln	
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ttt	gta	gta	tct	att	gca	gac	cgc	gat	atg	gtg	gct	cag	gtg	ctc	cgg	384
Phe	Val	Val	Ser	Ile	Ala	Asp	Arg	Asp	Met	Val	Ala	Gln	Val	Leu	Arg	
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gcg	gag	ggc	gct	gcg	ccc	cag	aga	gcc	aac	atg	gag	tcc	tgg	cgg	gag	432
Ala	Glu	Gly	Ala	Ala	Pro	Gln	Arg	Ala	Asn	Met	Glu	Ser	Trp	Arg	Glu	
	130					135					140					
tac	cga	gac	ttg	cgg	ggg	aga	gcc	acc	ggg	ctc	atc	tcg	gcg	gag	ggg	480
Tyr	Arg	Asp	Leu	Arg	Gly	Arg	Ala	Thr	Gly	Leu	Ile	Ser	Ala	Glu	Gly	
145					150					155					160	
gaa	cag	tgg	ctc	aag	atg	aga	agc	gta	ttg	aga	caa	aga	att	ctg	aaa	528
Glu	Gln	Trp	Leu	Lys	Met	Arg	Ser	Val	Leu	Arg	Gln	Arg	Ile	Leu	Lys	
				165					170					175		
ccg	aaa	gat	gtg	gcc	att	tat	tct	gga	gaa	gtc	gac	caa	gtt	att	gct	576
Pro	Lys	Asp	Val	Ala	Ile	Tyr	Ser	Gly	Glu	Val	Asp	Gln	Val	Ile	Ala	
			180					185					190			
gac	tta	att	aaa	aga	atc	tac	ctc	ctc	agg	agc	cag	gca	gaa	gat	gga	624
Asp	Leu	Ile	Lys	Arg	Ile	Tyr	Leu	Leu	Arg	Ser	Gln	Ala	Glu	Asp	Gly	
		195					200					205				
gaa	acc	gtg	acc	aat	gtc	aat	gat	ctt	ttc	ttc	aaa	tat	tca	atg	gaa	672
Glu	Thr	Val	Thr	Asn	Val	Asn	Asp	Leu	Phe	Phe	Lys	Tyr	Ser	Met	Glu	
	210					215					220					
gga	gtg	gcc	acc	atc	ctt	tat	gag	agt	cgt	ttg	ggc	tgc	ctg	gaa	aac	720
Gly	Val	Ala	Thr	Ile	Leu	Tyr	Glu	Ser	Arg	Leu	Gly	Cys	Leu	Glu	Asn	
225					230					235					240	
agc	atc	cca	cag	ctg	act	gtg	gaa	tac	atc	gag	gcc	ctg	gag	ctc	atg	768
Ser	Ile	Pro	Gln	Leu	Thr	Val	Glu	Tyr	Ile	Glu	Ala	Leu	Glu	Leu	Met	
				245					250					255		
ttt	agc	atg	ttc	aag	acc	tcc	atg	tat	gca	ggc	gcc	atc	ccc	aga	tgg	816
Phe	Ser	Met	Phe	Lys	Thr	Ser	Met	Tyr	Ala	Gly	Ala	Ile	Pro	Arg	Trp	
			260					265					270			
ctt	cgc	ccc	ttc	atc	cca	aag	ccc	tgg	cgg	gaa	ttc	tgc	agg	tcc	tgg	864
Leu	Arg	Pro	Phe	Ile	Pro	Lys	Pro	Trp	Arg	Glu	Phe	Cys	Arg	Ser	Trp	
			275				280					285				
gat	gga	ctc	ttc	aaa	ttc	agc	caa	att	cat	gtt	gac	aac	aag	ttg	tgg	912
Asp	Gly	Leu	Phe	Lys	Phe	Ser	Gln	Ile	His	Val	Asp	Asn	Lys	Leu	Trp	
	290					295					300					
gac	ata	cag	tac	caa	atg	gac	cga	ggc	cgg	agg	gtg	agc	ggg	gga	ctt	960
Asp	Ile	Gln	Tyr	Gln	Met	Asp	Arg	Gly	Arg	Arg	Val	Ser	Gly	Gly	Leu	

305	310	315	320	
ctc aca tac ctc ttc ctt agc cag gct ctg acg ctg cag gag atc tac				1008
Leu Thr Tyr Leu Phe Leu Ser Gln Ala Leu Thr Leu Gln Glu Ile Tyr				
325		330	335	
gcc aac gtg act gag atg ctg ctg gcc ggc gtc gac acg acg tcc ttc				1056
Ala Asn Val Thr Glu Met Leu Leu Ala Gly Val Asp Thr Thr Ser Phe				
340		345	350	
acc ttg tct tgg acg gtg tac ctc ctg gca agg cac cca gaa gtg cag				1104
Thr Leu Ser Trp Thr Val Tyr Leu Leu Ala Arg His Pro Glu Val Gln				
355		360	365	
cag acg gtg tac cgg gag att gtg aag aat tta ggg gaa agg cat gtt				1152
Gln Thr Val Tyr Arg Glu Ile Val Lys Asn Leu Gly Glu Arg His Val				
370		375	380	
cca act gca gct gat gtc ccc aag gtc ccg ctg gtc aga gct ctc ctt				1200
Pro Thr Ala Ala Asp Val Pro Lys Val Pro Leu Val Arg Ala Leu Leu				
385		390	395	400
aag gaa acc ctg agg ctg ttt cca gtg ctg cca ggg aac ggc cgg gtc				1248
Lys Glu Thr Leu Arg Leu Phe Pro Val Leu Pro Gly Asn Gly Arg Val				
405		410	415	
acc cag gaa gac ctg gtt att ggc ggg tat ctg att ccg aaa ggc acc				1296
Thr Gln Glu Asp Leu Val Ile Gly Gly Tyr Leu Ile Pro Lys Gly Thr				
420		425	430	
cag ctg gcc ctt tgc cac tat gcc aca tcg cac cag gat gag aac ttc				1344
Gln Leu Ala Leu Cys His Tyr Ala Thr Ser His Gln Asp Glu Asn Phe				
435		440	445	
cct cgg gcc aag gag ttc cga cct gag cgc tgg ctg cgg aaa gga gac				1392
Pro Arg Ala Lys Glu Phe Arg Pro Glu Arg Trp Leu Arg Lys Gly Asp				
450		455	460	
tta gat aga gtt gac aat ttt gga tcc atc ccc ttt ggt cat ggg gtt				1440
Leu Asp Arg Val Asp Asn Phe Gly Ser Ile Pro Phe Gly His Gly Val				
465		470	475	480
cgc agc tgc ata ggg cgg aga att gca gaa ctg gag att cac ctc gtc				1488
Arg Ser Cys Ile Gly Arg Arg Ile Ala Glu Leu Glu Ile His Leu Val				
485		490	495	
gtg atc cag ttg ctt caa cat ttt gag atc aaa aca tct tct cag acc				1536
Val Ile Gln Leu Leu Gln His Phe Gly Ile Lys Thr Ser Ser Gln Thr				
500		505	510	
aat gct gtt cat gca aaa acc cac ggg ctc ctg acg cca ggg ggg ccc				1584
Asn Ala Val His Ala Lys Thr His Gly Leu Leu Thr Pro Gly Gly Pro				
515		520	525	
atc cac gtg cga ttt gtt aac aga aag taa gcctagattt taaacctggg				1634
Ile His Val Arg Phe Val Asn Arg Lys *				
530		535		

ctgatgtagc agaccagctc gccgacacac agtgggtatt tgtgttcgct gatcacccgtg 1694  
gagaaggaaa gcgatgtcgc taaaggctgt cttgttatag actggcctcc caggctcctgg 1754  
gacacttgta aatctttatg caaagtaatg taaaaagggt gctattttac tgggtgcatac 1814  
cagaagttgc cctttctttg ggggaaacag ctgtttaaaa accagtggca gtgaattttt 1874  
atgcttcata cattngcta gactcaatat ttaatgactg gcagtatcct gtgcatttac 1934  
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<211> 537  
<212> PRT  
<213> Homo sapiens

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Ala Gly Ala Arg Leu Pro Ala Gly Ala Arg Ala Glu Asp Lys Gly Ala  
35 40 45  
Gly Arg Pro Gly Ser Pro Pro Gly Gly Gly Arg Ala Glu Gly Pro Arg  
50 55 60  
Ser Leu Ala Ala Met Pro Gly Pro Arg Thr Leu Ala Asn Leu Ala Glu  
65 70 75 80  
Phe Phe Cys Arg Asp Gly Phe Ser Arg Ile His Glu Ile Gln Gln Lys  
85 90 95  
His Thr Arg Glu Tyr Gly Lys Ile Phe Lys Ser His Phe Gly Pro Gln  
100 105 110  
Phe Val Val Ser Ile Ala Asp Arg Asp Met Val Ala Gln Val Leu Arg  
115 120 125  
Ala Glu Gly Ala Ala Pro Gln Arg Ala Asn Met Glu Ser Trp Arg Glu  
130 135 140  
Tyr Arg Asp Leu Arg Gly Arg Ala Thr Gly Leu Ile Ser Ala Glu Gly  
145 150 155 160  
Glu Gln Trp Leu Lys Met Arg Ser Val Leu Arg Gln Arg Ile Leu Lys  
165 170 175  
Pro Lys Asp Val Ala Ile Tyr Ser Gly Glu Val Asp Gln Val Ile Ala  
180 185 190  
Asp Leu Ile Lys Arg Ile Tyr Leu Leu Arg Ser Gln Ala Glu Asp Gly  
195 200 205  
Glu Thr Val Thr Asn Val Asn Asp Leu Phe Phe Lys Tyr Ser Met Glu  
210 215 220  
Gly Val Ala Thr Ile Leu Tyr Glu Ser Arg Leu Gly Cys Leu Glu Asn  
225 230 235 240  
Ser Ile Pro Gln Leu Thr Val Glu Tyr Ile Glu Ala Leu Glu Leu Met  
245 250 255  
Phe Ser Met Phe Lys Thr Ser Met Tyr Ala Gly Ala Ile Pro Arg Trp  
260 265 270  
Leu Arg Pro Phe Ile Pro Lys Pro Trp Arg Glu Phe Cys Arg Ser Trp  
275 280 285  
Asp Gly Leu Phe Lys Phe Ser Gln Ile His Val Asp Asn Lys Leu Trp  
290 295 300  
Asp Ile Gln Tyr Gln Met Asp Arg Gly Arg Arg Val Ser Gly Gly Leu  
305 310 315 320  
Leu Thr Tyr Leu Phe Leu Ser Gln Ala Leu Thr Leu Gln Glu Ile Tyr  
325 330 335  
Ala Asn Val Thr Glu Met Leu Leu Ala Gly Val Asp Thr Thr Ser Phe

	340		345		350
Thr Leu Ser Trp Thr Val Tyr Leu Leu Ala Arg His Pro Glu Val Gln					
	355		360		365
Gln Thr Val Tyr Arg Glu Ile Val Lys Asn Leu Gly Glu Arg His Val					
	370		375		380
Pro Thr Ala Ala Asp Val Pro Lys Val Pro Leu Val Arg Ala Leu Leu					
385		390		395	400
Lys Glu Thr Leu Arg Leu Phe Pro Val Leu Pro Gly Asn Gly Arg Val					
	405		410		415
Thr Gln Glu Asp Leu Val Ile Gly Gly Tyr Leu Ile Pro Lys Gly Thr					
	420		425		430
Gln Leu Ala Leu Cys His Tyr Ala Thr Ser His Gln Asp Glu Asn Phe					
	435		440		445
Pro Arg Ala Lys Glu Phe Arg Pro Glu Arg Trp Leu Arg Lys Gly Asp					
	450		455		460
Leu Asp Arg Val Asp Asn Phe Gly Ser Ile Pro Phe Gly His Gly Val					
465		470		475	480
Arg Ser Cys Ile Gly Arg Arg Ile Ala Glu Leu Glu Ile His Leu Val					
	485		490		495
Val Ile Gln Leu Leu Gln His Phe Glu Ile Lys Thr Ser Ser Gln Thr					
	500		505		510
Asn Ala Val His Ala Lys Thr His Gly Leu Leu Thr Pro Gly Gly Pro					
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Ile His Val Arg Phe Val Asn Arg Lys					
530		535			

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<211> 1614

<212> DNA

<213> Homo sapiens

<400> 3

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gcgcggggcg	aggacaaagg	cgccgggcg	ccggggtcgc	cgccgggagg	gggcccagcc	180
gaggggtccc	ggagcctcgc	cgccatgccg	gggcccagga	ccctcgccaa	cctggcgagg	240
ttcttctgca	gggacggctt	cagccgcata	cacgagatcc	agcagaagca	cacacgggaa	300
tatggaaaaa	tcttcaagtc	tcactttggt	cctcagtttg	tagtatctat	tgcagaccgc	360
gatatggtgg	ctcaggtgct	ccgggcggag	ggcgctgcgc	cccagagagc	caacatggag	420
tcttggcggg	agtaccgaga	cttgcggggg	agagccaccg	ggctcatctc	ggcgaggggg	480
gaacagtggc	tcaagatgag	aagcgtattg	agacaaagaa	ttctgaaacc	gaaagatgtg	540
gccatttatt	ctggagaagt	cgaccaagtt	attgctgact	taattaaaag	aatctacctc	600
ctcaggagcc	aggcagaaga	tggagaaacc	gtgaccaatg	tcaatgatct	tttcttcaaa	660
tattcaatgg	aaggagtggc	caccatcctt	tatgagagtc	gtttgggctg	cctggaaaac	720
agcatcccac	agctgactgt	ggaatacatc	gaggccctgg	agctcatggt	tagcatgttc	780
aagacctcca	tgtatgcagg	cgccatcccc	agatggcttc	gccccttcat	cccaaagccc	840
tggcgggaat	tctgcaggtc	ctgggatgga	ctcttcaa	tcagccaaat	tcatgttgac	900
aacaagttgt	gggacatata	gtaccaaagt	gaccgaggcc	ggaggggtgag	cgggggactt	960
ctcacatacc	tcttcccttag	ccaggctctg	acgctgcagg	agatctacgc	caacgtgact	1020
gagatgctgc	tggccggcgt	cgacacgacg	tccttcacct	tgtcttggac	ggtgtacctc	1080
ctggcaaggg	accagaagt	gcagcagacg	gtgtaccggg	agattgtgaa	gaatttaggg	1140
gaaaggcatg	ttccaactgc	agctgatgtc	cccaagggtcc	cgctgggtcag	agctctcctt	1200
aaggaaaccc	tgaggctggt	tccagtgtg	ccagggaacg	gccgggtcac	ccagggaagac	1260
ctggttattg	gcgggtatct	gattccgaaa	ggcacccagc	tggccctttg	ccactatgcc	1320
acatcgcacc	aggatgagaa	cttccctcgg	gccaaggagt	tccgacctga	gcgctggctg	1380
cggaaaggag	acttagatag	agttgacaat	tttggaacca	tcccctttgg	tcatgggggt	1440
cgcagctgca	tagggcgagg	aattgcagaa	ctggagattc	acctcgctcg	gatccagttg	1500

cttcaacatt ttgagatcaa aacatcttct cagaccaatg ctgttcatgc aaaaacccac 1560  
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 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Consensus amino acid sequence

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 Ala Lys Arg Tyr Gly Lys Pro Val Phe Thr Leu Tyr Leu Gly Pro Arg  
 35 40 45  
 Pro Val Val Val Leu Thr Gly Pro Glu Ala Val Lys Glu Val Leu Ile  
 50 55 60  
 Asp Lys Gly Glu Glu Phe Ala Lys Gly Arg Gly Asp Phe Asn Pro Thr  
 65 70 75 80  
 Phe Pro Trp Leu Ser Lys Gly Tyr Arg Glu Gln Gly Leu Leu Phe Ser  
 85 90 95  
 Asp Asn Gly Pro Lys Trp Arg Lys Leu Arg Arg Phe Ser Leu Leu Thr  
 100 105 110  
 Leu Arg Phe His Phe Gly Met Gly Ala Tyr Ser Lys Arg Ser Gln Lys  
 115 120 125  
 Leu Glu Glu Pro Arg Ile Gln Glu Glu Ala Arg Asp Leu Val Glu Arg  
 130 135 140  
 Leu Arg Lys Glu Gln Ala Gly Ser Pro Ile Asp Ile Thr Glu Leu Leu  
 145 150 155 160  
 Ala Arg Leu Ala Pro Leu Asn Val Ile Cys Ser Leu Leu Phe Gly Val  
 165 170 175  
 Arg Phe Asp Tyr Leu Arg Pro Glu Asp Pro Glu Phe Leu Lys Leu Ile  
 180 185 190  
 Asp Lys Leu Leu Asn Glu Met Phe Asp Arg Val Ser Pro Trp His Gln  
 195 200 205  
 Leu Leu Asp Ile Phe Pro Phe Leu Leu Arg Tyr Leu Pro Gly Ser Leu  
 210 215 220  
 Phe Arg Lys Ala Phe Lys Ala Ala Lys Asp Leu Lys Asp Tyr Leu Asp  
 225 230 235 240  
 Lys Leu Ile Glu Glu Arg Arg Glu Thr Leu Glu Pro Ala Gly Asp Pro  
 245 250 255  
 Arg Arg Leu Asp Ile Gly Phe Leu Asp Ser Leu Leu Leu Glu Ala Lys  
 260 265 270  
 Arg Glu Gly Gly Asn Pro Lys Ser Glu Leu Ser Asp Glu Glu Leu Ala  
 275 280 285  
 Ala Thr Val Leu Asp Leu Leu Phe Ala Gly Thr Glu Thr Thr Ser Ser  
 290 295 300  
 Thr Leu Ser Trp Ala Leu Tyr Leu Leu Ala Lys His Pro Glu Val Gln  
 305 310 315 320  
 Ala Lys Leu Arg Glu Glu Ile Asp Glu Val Ile Gly Arg Asp Arg Ser  
 325 330 335  
 Pro Thr Tyr Asp Val Asp Ala Arg Ala Gln Met Pro Tyr Leu Asp Ala  
 340 345 350  
 Val Ile Lys Glu Thr Leu Arg Leu Tyr Pro Val Val Pro Leu Leu Leu



<400> 6

Gly Leu Pro Val Val Gly Thr Leu Val Asp Leu Ile Ala Ala Gly Gly  
1 5 10 15  
Ala Thr His Leu His Lys Tyr Ile Asp Ala Arg His Lys Gln Tyr Gly  
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35 40 45  
Ser Ser Ala Asn Leu Met Arg Gly Val Phe Gln His Glu Gly Gln Tyr  
50 55 60  
Pro Gln His Pro Leu Pro Asp Ala Trp Thr Leu Tyr Asn Gln Gln His  
65 70 75 80  
Ala Cys Gln Arg Gly Leu Phe Phe Met Glu Gly Ala Glu Trp Leu His  
85 90 95  
Asn Arg Arg Ile Leu Asn Arg Leu Leu Leu Asn Gly Asn Leu Asn Trp  
100 105 110  
Met Asp Val His Ile Glu Ser Cys Thr Arg Arg Met Val Asp Gln Trp  
115 120 125  
Lys Arg Arg Thr Ala Glu Ala Ala Ala Ile Pro Leu Ala Glu Ser Gly  
130 135 140  
Glu Ile Arg Ser Tyr Glu Leu Pro Leu Leu Glu Gln Gln Leu Tyr Arg  
145 150 155 160  
Trp Ser Ile Glu Val Leu Cys Cys Ile Met Phe Gly Thr Ser Val Leu  
165 170 175  
Thr Cys Pro Lys Ile Gln Ser Ser Leu Asp Tyr Phe Thr Gln Ile Val  
180 185 190  
His Lys Val Phe Glu His Ser Ser Arg Leu Met Thr Phe Pro Pro Arg  
195 200 205  
Leu Ala Gln Ile Leu Arg Leu Pro Ile Trp Arg Asp Phe Glu Ala Asn  
210 215 220  
Val Asp Glu Val Leu Arg Glu Gly Ala Ala Ile Ile Asp His Cys Ile  
225 230 235 240  
Arg Val Gln Glu Asp Gln Arg Arg Pro His Asp Glu Ala Leu Tyr His  
245 250 255  
Arg Leu Gln Ala Ala Asp Val Pro Gly Asp Met Ile Lys Arg Ile Phe  
260 265 270  
Val Asp Leu Val Ile Ala Ala Gly Asp Thr Thr Ala Phe Ser Ser Gln  
275 280 285  
Trp Ala Leu Phe Ala Leu Ser Lys Glu Pro Arg Leu Gln Gln Arg Leu  
290 295 300  
Ala Lys Glu Arg Ala Thr Asn Asp Ser Arg Leu Met His Gly Leu Ile  
305 310 315 320  
Lys Glu Ser Leu Arg Leu Tyr  
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<211> 87

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 7

Leu Ala Asp Ile Pro Gly Pro Gly Thr Leu Arg Phe Leu Phe Gln Leu  
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Phe Cys Lys Gly Tyr Leu Leu His Leu His Glu Leu Gln Val Leu Gly



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Lys	Ala	Arg	Tyr	Gly	Pro	Met	Trp	Met	Ser	Ser	Phe	Gly	Thr	Gln	Arg	
		35					40					45				
Thr	Val	Asn	Leu	Ala	Ser	Pro	Pro	Leu	Val	Glu	Gln	Val	Met	Arg	Gln	
	50					55					60					
Glu	Gly	Lys	Tyr	Pro	Val	Arg	Cys	Ser	Phe	Glu	Pro	Trp	Lys	Glu	His	
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Arg	Arg	Arg	His	Gln	Arg	Ala										
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<220>  
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Arg	Leu	His	Pro	Pro	Val	Pro	Thr	Val	Met	Arg	Lys	Val	Lys	Lys	Asp	
			20					25					30			
Met	Glu	Val	Ser	Gly	Thr	Val	Gly	Gly	Glu	Tyr	Thr	Ile	Pro	Lys	Gly	
		35				40						45				
Thr	Gln	Val	Met	Val	Ser	Pro	Tyr	Val	Met	Thr	His	Arg	Asp	Pro	Glu	
	50				55						60					
Tyr	Tyr	Pro	Asp	Pro	Glu	Glu	Phe	Asn	Pro	Glu	Arg	Trp	Leu	Glu	Pro	
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Ser	Glu															

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Ile	Ile	Ile	Ala	Glu	Ala	Glu	Leu	Cys	Arg	Glu	Val	Gly	Ile	Lys	Lys	
			20					25					30			
Phe	Lys	Asp	Leu	Pro	Asn	Arg	Ser	Ile	Pro	Ser	Pro	Ile	Ser	Ala	Ser	
		35					40					45				
Pro	Leu	His	Lys	Lys	Gly	Leu	Phe	Phe	Thr	Arg	Asp	Lys	Arg	Trp	Ser	
	50				55						60					
Lys	Met	Arg	Asn	Thr	Ile	Leu	Ser	Leu	Tyr	Gln	Pro	Ser	His	Leu	Thr	
65				70						75					80	
Ser	Leu	Ile	Pro	Thr	Met	His	Ser	Phe	Ile	Thr	Ser	Ala	Thr	His	Asn	
				85					90					95		
Leu	Asp	Ser	Lys	Pro	Arg	Asp	Ile	Val	Phe	Ser	Asn	Leu	Phe	Leu	Lys	
			100					105					110			
Leu	Thr	Thr	Asp	Ile	Ile	Gly	Gln	Ala	Ala	Phe	Gly	Val	Asp	Phe	Gly	
		115					120						125			

Leu	Ser	Gly	Lys	Lys	Pro	Ile	Lys	Asp	Val	Glu	Val	Thr	Asp	Phe	Ile
130						135					140				
Asn	Gln	His	Val	Tyr	Ser	Thr	Thr	Gln	Leu	Lys	Met	Asp	Leu	Ser	Gly
145				150						155					160
Ser	Leu	Ser	Ile	Ile	Leu	Gly	Leu	Leu	Ile	Pro	Ile	Leu	Gln	Glu	Pro
			165						170					175	
Phe	Arg	Gln	Val	Leu	Lys	Arg	Ile	Pro	Gly	Thr	Met	Asp	Trp	Arg	Val
			180					185					190		
Glu	Lys	Thr	Asn	Ala	Arg	Leu	Ser	Gly	Gln	Leu	Asn	Glu	Ile	Val	Ser
		195					200					205			
Lys	Arg	Ala	Lys	Glu	Ala	Glu	Thr	Asp	Ser	Lys	Asp	Phe	Leu	Ser	Leu
	210					215					220				
Ile	Leu	Lys	Ala	Arg	Glu	Ser	Asp	Pro	Phe	Ala	Lys	Asn	Ile	Phe	Thr
225				230						235					240
Ser	Asp	Tyr	Ile	Ser	Ala	Val	Thr	Tyr	Glu	His	Leu	Leu	Ala	Gly	Ser
			245						250					255	
Ala	Thr	Thr	Ala	Phe	Thr	Leu	Ser	Ser	Val	Leu	Tyr	Leu	Val	Ser	Gly
			260					265					270		
His	Leu	Asp	Val	Glu	Lys	Arg	Leu	Leu	Gln	Glu	Ile	Asp	Gly	Phe	Gly
		275					280					285			
Asn	Arg	Asp	Leu	Ile	Pro	Thr	Ala	His	Asp	Leu	Gln	His	Lys	Phe	Pro
	290					295					300				
Tyr	Leu	Asp	Gln	Val	Ile	Lys	Glu	Ala	Met	Arg	Phe	Tyr	Met	Val	
305					310					315					

<210> 10

<211> 138

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 10

Ala	Ile	Pro	Gly	Pro	Arg	Gly	Pro	Phe	Gly	Met	Gly	Asn	Leu	Tyr	Asn
1				5					10					15	
Tyr	Leu	Pro	Gly	Ile	Gly	Ser	Tyr	Ser	Trp	Leu	Arg	Leu	His	Gln	Ala
			20				25						30		
Gly	Gln	Asp	Lys	Tyr	Glu	Lys	Tyr	Gly	Ala	Ile	Val	Arg	Glu	Thr	Ile
		35				40					45				
Val	Pro	Gly	Gln	Asp	Ile	Val	Trp	Leu	Tyr	Asp	Pro	Lys	Asp	Ile	Ala
	50					55				60					
Leu	Leu	Leu	Asn	Glu	Arg	Asp	Cys	Pro	Gln	Arg	Arg	Ser	His	Leu	Ala
65					70				75					80	
Leu	Ala	Gln	Tyr	Arg	Lys	Ser	Arg	Pro	Asp	Val	Tyr	Lys	Thr	Thr	Gly
			85						90				95		
Leu	Leu	Pro	Thr	Asn	Gly	Pro	Glu	Trp	Trp	Arg	Ile	Arg	Ala	Gln	Val
		100					105						110		
Gln	Lys	Glu	Leu	Ser	Ala	Pro	Lys	Ser	Val	Arg	Asn	Phe	Val	Arg	Gln
	115					120					125				
Val	Asp	Gly	Val	Thr	Lys	Glu	Phe	Ile	Arg						
130						135									

<210> 11

<211> 302

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 11

Thr	Glu	Leu	Tyr	Asp	Leu	Tyr	Ile	Arg	Glu	Ser	Met	Glu	Lys	Tyr	Gly
1				5					10					15	
Ala	Val	Lys	Phe	Phe	Phe	Gly	Ser	Arg	Trp	Asn	Ile	Leu	Val	Ser	Arg
			20					25					30		
Ser	Glu	Tyr	Leu	Ala	Gln	Ile	Phe	Lys	Asp	Glu	Asp	Thr	Phe	Ala	Lys
		35					40					45			
Ser	Gly	Asn	Gln	Lys	Lys	Ile	Pro	Tyr	Ser	Ala	Leu	Ala	Ala	Tyr	Thr
	50					55					60				
Gly	Asp	Asn	Val	Ile	Ser	Ala	Tyr	Gly	Ala	Val	Trp	Arg	Asn	Tyr	Arg
65				70						75				80	
Asn	Ala	Val	Thr	Asn	Gly	Leu	Gln	His	Phe	Asp	Asp	Ala	Pro	Ile	Phe
				85					90					95	
Lys	Asn	Ala	Lys	Ile	Leu	Cys	Thr	Leu	Ile	Lys	Asn	Arg	Leu	Leu	Glu
			100					105					110		
Gly	Gln	Thr	Ser	Ile	Pro	Met	Gly	Pro	Leu	Ser	Gln	Arg	Met	Ala	Leu
		115					120					125			
Asp	Asn	Ile	Ser	Gln	Val	Ala	Leu	Gly	Phe	Asp	Phe	Gly	Ala	Leu	Thr
	130					135					140				
His	Glu	Lys	Asn	Ala	Phe	His	Glu	His	Leu	Ile	Arg	Ile	Lys	Lys	Gln
145				150						155				160	
Ile	Phe	His	Pro	Phe	Phe	Leu	Thr	Phe	Pro	Phe	Leu	Asp	Val	Leu	Pro
				165					170					175	
Ile	Pro	Ser	Arg	Lys	Lys	Ala	Phe	Lys	Asp	Val	Val	Ser	Phe	Arg	Glu
		180						185					190		
Leu	Leu	Val	Lys	Arg	Val	Gln	Asp	Glu	Leu	Val	Asn	Asn	Tyr	Lys	Phe
		195					200					205			
Glu	Gln	Thr	Thr	Phe	Ala	Ala	Ser	Asp	Leu	Ile	Arg	Ala	His	Asn	Asn
	210					215					220				
Glu	Ile	Ile	Asp	Tyr	Lys	Gln	Leu	Thr	Asp	Asn	Ile	Val	Ile	Ile	Leu
225				230						235				240	
Val	Ala	Gly	His	Glu	Asn	Pro	Gln	Leu	Leu	Phe	Asn	Ser	Ser	Leu	Tyr
			245						250					255	
Leu	Leu	Ala	Lys	Tyr	Ser	Asn	Glu	Trp	Gln	Glu	Lys	Leu	Arg	Lys	Glu
		260						265					270		
Val	Asn	Gly	Ile	Thr	Asp	Pro	Lys	Gly	Leu	Ala	Asp	Leu	Pro	Leu	Leu
	275					280						285			
Asn	Ala	Phe	Leu	Phe	Glu	Val	Val	Arg	Met	Tyr	Pro	Pro	Leu		
	290					295					300				

<210> 12

<211> 138

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 12

Leu	Arg	Gln	Val	Gln	Asp	Glu	Thr	Ile	Arg	Leu	Ser	Thr	Leu	Ala	Pro
1				5					10					15	
Trp	Ala	Ala	Arg	Tyr	Ser	Asp	Lys	Lys	Val	Thr	Val	Cys	Gly	Tyr	Thr
			20					25					30		

Ile	Pro	Ala	Lys	Thr	Pro	Met	Ile	His	Ala	Leu	Gly	Val	Gly	Leu	Lys
		35					40					45			
Asn	Lys	Thr	Val	Trp	Glu	Asn	Thr	Asp	Ser	Trp	Asp	Pro	Asp	Arg	Phe
	50					55					60				
Ser	Pro	Asn	Gly	Arg	Arg	Gly	Asn	Asp	Phe	Cys	Pro	Phe	Gly	Val	His
65					70					75				80	
Ser	Arg	Arg	Lys	Cys	Pro	Gly	Tyr	Leu	Phe	Ser	Tyr	Phe	Glu	Val	Gly
			85						90					95	
Val	Phe	Ala	Ser	Ile	Leu	Leu	Ser	Arg	Phe	Glu	Ile	Val	Pro	Val	Glu
		100					105						110		
Gly	Gln	Thr	Val	Ile	Gln	Val	His	Gly	Leu	Val	Thr	Glu	Pro	Lys	Asp
	115					120						125			
Asp	Ile	Lys	Ile	Tyr	Ile	Arg	Ser	Arg	Lys						
	130					135									

<210> 13

<211> 67

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 13

Ile	Ala	Gly	Met	Asp	Thr	Ala	Ala	Asn	Ser	Leu	Ala	Phe	Val	Leu	Tyr
1				5					10					15	
Arg	Met	His	Leu	His	Ser	Glu	Phe	Leu	Pro	Ala	Leu	Arg	Ala	Glu	Ala
		20					25						30		
Asp	Ala	Leu	Phe	Arg	Asp	Gly	Pro	Pro	Thr	Ala	Glu	Ala	Leu	Gly	Arg
	35					40					45				
Ser	Pro	Leu	Leu	His	Arg	Phe	Val	Met	Glu	Thr	Leu	Arg	Val	His	Pro
	50				55						60				
Ile	Ala	Pro													
65															

<210> 14

<211> 95

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 14

Val	Pro	Ala	Pro	Pro	Phe	Leu	Gly	His	Ala	Ala	Glu	Met	Gly	Thr	Ile
1				5					10					15	
Lys	Leu	Arg	Pro	Phe	Leu	Thr	Arg	Cys	Tyr	Gln	Ala	Tyr	Gly	Pro	Val
		20					25						30		
Phe	Gln	Leu	Thr	Val	Pro	Gly	Gln	Lys	Ile	Thr	Val	Leu	Ala	Gly	Pro
	35					40					45				
Glu	Ala	Asn	Leu	Phe	Ala	Met	Lys	Glu	Gly	His	Arg	Val	Leu	Arg	Ser
	50				55					60					
Leu	Glu	Ala	Trp	Arg	Asp	Asn	Asp	His	Glu	Met	Gly	Ser	Asp	Arg	Ser
65				70					75					80	
Met	Ile	Ser	Leu	Asp	Gly	Ala	Glu	His	Arg	Ala	Tyr	Arg	Arg	Val	
			85					90						95	

<210> 15  
 <211> 131  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Consensus amino acid sequence

<400> 15  
 Thr Val Ala Ile Ser Pro Tyr Gly Glu Gln Trp Lys Lys Met Arg Lys  
 1 5 10 15  
 Val Ile Thr Thr Glu Ile Met Ser Pro Lys Arg Leu Asn Trp Leu Leu  
 20 25 30  
 Gly Lys Arg Thr Glu Glu Ala Asp Asn Leu Val Ala Tyr Val His Asn  
 35 40 45  
 Met Cys Gln Lys Ser Glu Thr Asn Asn Lys His Gly Ala Val Ile Asp  
 50 55 60  
 Val Arg Asp Val Val Arg His Tyr Cys His Asn Val Val Met Arg Met  
 65 70 75 80  
 Met Phe Gly Arg Arg His Phe Gly Lys Gly Thr Glx Phe Ser Asp Asp  
 85 90 95  
 Gly Gly Pro Gly Pro Glu Glu Lys Glu His Met Asp Ala Ile Phe Thr  
 100 105 110  
 Ala Leu Asp Cys Leu Tyr Ala Phe Cys Val Ser Asp Tyr Ile Pro Arg  
 115 120 125  
 Trp Leu Arg  
 130

<210> 16  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Consensus amino acid sequence

<400> 16  
 Arg Trp Leu Arg Gly Trp Asp Leu Asp  
 1 5